



HR - Skin2.ST25
SEQUENCE LISTING

<110> The Procter & Gamble Company

<120> Hairless Protein-Interacting Partner Complexes And Methods Thereof For The Beautification And/Or Improvement Of Mammalian Skin

<130> 9423

<160> 16

<170> PatentIn version 3.2

<210> 1

<211> 660

<212> DNA

<213> Homo Sapiens Keratin 5

<400> 1

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<210> 2

<211> 746

<212> DNA

<213> Homo Sapiens Ubiquitous Receptor

<400> 2

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<211> 705
<212> DNA
<213> Homo Sapiens Protein Inhibitor of Activated STAT-1

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<210> 4
<211> 792
<212> DNA
<213> Homo Sapiens Similar to Stromal Antigen 2

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	tactctgtag	atgcagaaaa	ggtgactaac	ttgttgca	tgcctcagta	ctttgattt	240
	gaaatatata	ccactggacg	attagaaaag	catttggatg	ccttattgcg	acagatccgg	300
	aatattgtag	agaagcacac	agatacagat	gttttggaa	catgttctaa	aacttaccat	360
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atacatgtat tggcagataa atttaccgg cttcttgaag atttctgca agagggtgaa	480
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cataatgccc atgaccttc aaagtggat ttatttgctt gtaattacaa actcttgaaa	600
actggaatcg aaaatggaga catgcctgag cagattgtt ttcacgcact gcagtgtact	660
cactatgtaa tccttggca acttgctaag ataactgaaa gcagctctac aaaggaggac	720
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aacgtgaata ct	792

<210> 5

<211> 747

<212> DNA

<213> Homo Sapiens Nucleoporin 160 kda

<400> 5

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agcaggcaat tagattgtt acggcagttg gtggtagttc tttgtgaacg ctcacagcta	180
caggatctt tagagtttcc ctatgtaat ctgcataatg aggttgtgg aataatttag	240
tcacgtgcta gagctgtgga ccttatgact cacaattact atgaacttct gtatgcctt	300
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<210> 6

<211> 683

<212> DNA

<213> Homo Sapiens Retinoic Acid Receptor Gamma-1

<400> 6

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ggggctgtgg ctgaagacct cgcccgcccc ctgcagaccc caggggactc tcacaccgca	180
gctgccatgg ccaccaataa ggagcgactc tttgcggctg gtgcctggg gcctggatct	240

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ggctacccag	gggcagggtt	ccccttcgcc	ttcccagggg	cactcagggg	gtctccgcct	300
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<210> 7
<211> 744
<212> DNA
<213> Homo Sapiens Thyroid Hormone Receptor Alpha

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	gacaagggtgg	accttggaaagc	tttcagcgcag	tttaccaaga	tcatcacccc	ggccatcacc	660
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<210> 8
<211> 719
<212> DNA
<213> Homo Sapiens Annexin A1

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	ccagcgcaat	ttgatgctga	tgaacttcgt	gctgccatga	aggccttgg	aactgatgaa	180
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<210> 9

<211> 323

<212> DNA

<213> Homo Sapiens HIC Protein Isoform P32 and Isoform 40

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ctaccaatag ccacttcaca catggagaga tgcaagacca gtccatttgg ggaaatcctt	180
cggatgtga actcattaga acccaacctc agcgcttgc tcagcttcag acttcagcac	240
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<210> 10

<211> 610

<212> DNA

<213> Homo Sapiens Insulin-like Growth Factor Binding Domain Protein 6

<400> 10

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<210> 11
<211> 718
<212> DNA
<213> Homo Sapiens Inner Membrane Protein, Mitochondrial

<400> 11		
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<210> 12
<211> 720
<212> DNA
<213> Homo Sapiens Endoplasmic reticulum thioredoxin superfamily member

<400> 12		
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<210> 13
<211> 779
<212> DNA
<213> Homo Sapiens Protein Inhibitor of Activated STAT-3

<400> 13
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<210> 14
<211> 738
<212> DNA
<213> Homo Sapiens DEAD box polypeptide 3

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cgctcaggaa	aaagccca					738											
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<211> 450																	
<212> DNA																	
<213> Homo Sapiens Dpy-30 Like Protein																	
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Asp	Arg	Asn	Val	Pro	Arg	Ile	Cys	Gly	Val	Cys	Gly	Asp	Arg	Ala	Thr		
			20				25									30	
Gly	Phe	His	Phe	Asn	Ala	Met	Thr	Cys	Glu	Gly	Cys	Lys	Gly	Phe	Phe		
			35				40									45	
Arg	Arg	Ser	Met	Lys	Arg	Lys	Ala	Leu	Phe	Thr	Cys	Pro	Phe	Asn	Gly		
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Asp	Cys	Arg	Ile	Thr	Lys	Asp	Asn	Arg	Arg	His	Cys	Gln	Ala	Cys	Arg		
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Leu	Lys	Arg	Cys	Val	Asp	Ile	Gly	Met	Met	Lys	Glu	Phe	Ile	Leu	Thr		
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Asp	Glu	Glu	Val	Gln	Arg	Lys	Arg	Glu	Met	Ile	Met	Lys	Arg	Lys	Glu		
			100				105									110	

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Glu Glu Ala Leu Lys Asp Ser Leu Arg Pro Lys Leu Ser Glu Glu Gln
115 120 125

Gln His Ile Ile Ala Ile Leu Leu Asp Ala His His Lys Thr Tyr Asp
130 135 140

Pro Thr Tyr Ala Asp Phe Arg Asp Phe Arg Pro Pro Ile Arg Ala Asp
145 150 155 160

Val Ser Thr Gly Ser Tyr Ser Pro Arg Pro Thr Leu Ser Phe Ser Gly
165 170 175

Asp Ser Ser Ser Asn Ser Asp Leu Tyr Thr Pro Ser Leu Asp Met Met
180 185 190

Glu Pro Ala Ser Phe Ser Thr Met Asp Leu Asn Glu Glu Gly Ser Asp
195 200 205

Asp Pro Ser Val Thr Leu Asp Leu Ser Pro Leu Ser Met Leu Pro His
210 215 220

Leu Ala Asp Leu Val Ser Tyr Ser Ile Gln Lys Val Ile Gly Phe Ala
225 230 235 240

Lys Met Ile Pro Gly Phe Arg Asp Leu Thr Ser Asp Asp Gln Ile Val
245 250 255

Leu Leu Lys Ser Ser Ala Ile Glu Val Ile Met Leu Arg Ser Asn Gln
260 265 270

Ser Phe Thr Leu Asp Asp Met Ser Trp Asp Cys Gly Ser Gln Asp Tyr
275 280 285

Lys Tyr Asp Ile Thr Asp Val Ser Arg Ala Gly His Thr Leu Glu Leu
290 295 300

Ile Glu Pro Leu Ile Lys Phe Gln Val Gly Leu Lys Lys Leu Asn Leu
305 310 315 320

His Glu Glu Glu His Val Leu Leu Met Ala Ile Cys Ile Val Ser Pro
325 330 335

Asp Arg Pro Gly Val Gln Asp Ala Lys Leu Val Glu Ala Ile Gln Asp
340 345 350

Arg Leu Ser Asn Thr Leu Gln Thr Tyr Ile Arg Cys Arg His Pro Pro
355 360 365

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Pro Gly Ser His Gln Leu Tyr Ala Lys Met Ile Gln Lys Leu Ala Asp
370 375 380

Leu Arg Ser Leu Asn Glu Glu His Ser Lys Gln Tyr Arg Ser Leu Ser
385 390 395 400

Phe Gln Pro Glu Asn Ser Met Lys Leu Thr Pro Leu Val Leu Glu Val
405 410 415

Phe Gly Asn Glu Ile Ser
420